SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ashkenazi et al.

(ii) TITLE OF INVENTION: RTD Receptor

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Genentech, Inc.
 (B) STREET: 1 DNA Way
 (C) CITY: South San Francisco
 (D) STATE: California
 (E) COUNTRY: USA
 (F) ZIP: 94080

(v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Marschang, Diane L.
 (B) REGISTRATION NUMBER: 35,600
 (C) REFERENCE/DOCKET NUMBER: P1129

(ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 650/225-5416
 (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 386 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg
1   5   10   15

Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro
                20   25   30

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              Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val
                           35              40                  45

              Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg
      5                    50              55                  60

              Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
                           65              70                  75

      10      Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser
                           80              85                  90

              Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
                           95             100                 105
      15
              Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val
                          110             115                 120

              Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg
      20                   125             130                 135

              Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn
                          140             145                 150

      25      Ser Pro Glu Met Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly
                          155             160                 165

              Met Val Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
      30                   170             175                 180

              Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro Ala Ala
                          185             190                 195

              Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu Ala Ser Pro Tyr
      35                   200             205                 210

              His Tyr Leu Ile Ile Ile Val Val Leu Val Ile Ile Leu Ala Val
                          215             220                 225

      40      Val Val Val Gly Phe Ser Cys Arg Lys Lys Phe Ile Ser Tyr Leu
                          230             235                 240

              Lys Gly Ile Cys Ser Gly Gly Gly Gly Gly Pro Glu Arg Val His
                          245             250                 255
      45
              Arg Val Leu Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly
                          260             265                 270

              Ala Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr Leu
      50                   275             280                 285

              Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly Gln Glu Leu
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                    ●                              ●

             290                    295                    300
    Ala Glu Leu Thr Gly Val Thr Val Glu Xaa Pro Glu Glu Pro Gln
                 305                    310                    315
    Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg
                 320                    325                    330
    Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr
                 335                    340                    345
    Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu
                 350                    355                    360
    Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
                 365                    370                    375
    Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
                 380                385 386
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(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2082 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CCAACTGCAC CTCGGTTCTA TCGATTGAAT TCCCCGGGGA TCCTCTAGAG  50

ATCCCTCGAC CTCGACCCAC GCGTCCGGAA CCTTTGCACG CGCACAAACT 100

ACGGGGACGA TTTCTGATTG ATTTTTGGCG CTTTCGATCC ACCCTCCTCC 150

CTTCTC  ATG GGA CTT TGG GGA CAA AGC GTC CCG ACC GCC 189
        Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala
         1               5                  10

TCG AGC GCT CGA GCA GGG CGC TAT CCA GGA GCC AGG ACA 228
Ser Ser Ala Arg Ala Gly Arg Tyr Pro Gly Ala Arg Thr
             15                  20

GCG TCG GGA ACC AGA CCA TGG CTC CTG GAC CCC AAG ATC 267
Ala Ser Gly Thr Arg Pro Trp Leu Leu Asp Pro Lys Ile
 25              30                  35

CTT AAG TTC GTC GTC TTC ATC GTC GCG GTT CTG CTG CCG 306
Leu Lys Phe Val Val Phe Ile Val Ala Val Leu Leu Pro
         40                  45                  50
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GTC CGG GTT GAC TCT GCC ACC ATC CCC CGG CAG GAC GAA 345
Val Arg Val Asp Ser Ala Thr Ile Pro Arg Gln Asp Glu
                    55   60

GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG AGG CGC 384
Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg Arg
        65   70   75

AGC CTC AAG GAG GAG GAG TGT CCA GCA GGA TCT CAT AGA 423
Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg
                80   85

TCA GAA TAT ACT GGA GCC TGT AAC CCG TGC ACA GAG GGT 462
Ser Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
    90   95   100

GTG GAT TAC ACC ATT GCT TCC AAC AAT TTG CCT TCT TGC 501
Val Asp Tyr Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys
            105   110   115

CTG CTA TGT ACA GTT TGT AAA TCA GGT CAA ACA AAT AAA 540
Leu Leu Cys Thr Val Cys Lys Ser Gly Gln Thr Asn Lys
                120   125

AGT TCC TGT ACC ACG ACC AGA GAC ACC GTG TGT CAG TGT 579
Ser Ser Cys Thr Thr Thr Arg Asp Thr Val Cys Gln Cys
        130   135   140

GAA AAA GGA AGC TTC CAG GAT AAA AAC TCC CCT GAG ATG 618
Glu Lys Gly Ser Phe Gln Asp Lys Asn Ser Pro Glu Met
                145   150

TGC CGG ACG TGT AGA ACA GGG TGT CCC AGA GGG ATG GTC 657
Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly Met Val
155   160   165

AAG GTC AGT AAT TGT ACG CCC CGG AGT GAC ATC AAG TGC 696
Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
            170   175   180

AAA AAT GAA TCA GCT GCC AGT TCC ACT GGG AAA ACC CCA 735
Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro
                185   190

GCA GCG GAG GAG ACA GTG ACC ACC ATC CTG GGG ATG CTT 774
Ala Ala Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu
    195   200   205

GCC TCT CCC TAT CAC TAC CTT ATC ATC ATA GTG GTT TTA 813
Ala Ser Pro Tyr His Tyr Leu Ile Ile Ile Val Val Leu
            210   215

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GTC ATC ATT TTA GCT GTG GTT GTG GTT GGC TTT TCA TGT 852
Val Ile Ile Leu Ala Val Val Val Val Gly Phe Ser Cys
220   225   230

CGG AAG AAA TTC ATT TCT TAC CTC AAA GGC ATC TGC TCA 891
Arg Lys Lys Phe Ile Ser Tyr Leu Lys Gly Ile Cys Ser
        235   240   245

GGT GGT GGA GGA GGT CCC GAA CGT GTG CAC AGA GTC CTT 930
Gly Gly Gly Gly Gly Pro Glu Arg Val His Arg Val Leu
                250   255

TTC CGG CGG CGT TCA TGT CCT TCA CGA GTT CCT GGG GCG 969
Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly Ala
    260   265   270

GAG GAC AAT GCC CGC AAC GAG ACC CTG AGT AAC AGA TAC 1008
Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr
            275   280

TTG CAG CCC ACC CAG GTC TCT GAG CAG GAA ATC CAA GGT 1047
Leu Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly
285   290   295

CAG GAG CTG GCA GAG CTA ACA GGT GTG ACT GTA GAG TYG 1086
Gln Glu Leu Ala Glu Leu Thr Gly Val Thr Val Glu Xaa
        300   305   310

CCA GAG GAG CCA CAG CGT CTG CTG GAA CAG GCA GAA GCT 1125
Pro Glu Glu Pro Gln Arg Leu Leu Glu Gln Ala Glu Ala
            315   320

GAA GGG TGT CAG AGG AGG AGG CTG CTG GTT CCA GTG AAT 1164
Glu Gly Cys Gln Arg Arg Arg Leu Leu Val Pro Val Asn
        325   330   335

GAC GCT GAC TCC GCT GAC ATC AGC ACC TTG CTG GAT GCC 1203
Asp Ala Asp Ser Ala Asp Ile Ser Thr Leu Leu Asp Ala
            340   345

TCG GCA ACA CTG GAA GAA GGA CAT GCA AAG GAA ACA ATT 1242
Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu Thr Ile
350   355   360

CAG GAC CAA CTG GTG GGC TCC GAA AAG CTC TTT TAT GAA 1281
Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
        365   370   375

GAA GAT GAG GCA GGC TCT GCT ACG TCC TGC CTG TGAAAG 1320
Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
            380   385 386

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AATCTCTTCA GGAAACCAGA GCTTCCCTCA TTTACCTTTT CTCCTACAAA 1370

GGGAAGCAGC CTGGAAGAAA CAGTCCAGTA CTTGACCCAT GCCCCAACAA 1420

ACTCTACTAT CCAATATGGG GCAGCTTACC AATGGTCCTA GAACTTTGTT 1470

AACGCACTTG GAGTAATTTT TATGAAATAC TGCGTGTGAT AAGCAAACGG 1520

GAGAAATTTA TATCAGATTC TTGGCTGCAT AGTTATACGA TTGTGTATTA 1570

AGGGTCGTTT TAGGCCACAT GCGGTGGCTC ATGCCTGTAA TCCCAGCACT 1620

TTGATAGGCT GAGGCAGGTG GATTGCTTGA GCTCGGGAGT TTGAGACCAG 1670

CCTCATCAAC ACAGTGAAAC TCCATCTCAA TTTAAAAGA AAAAAAGTGG 1720

TTTTAGGATG TCATTCTTTG CAGTTCTTCA TCATGAGACA AGTCTTTTTT 1770

TCTGCTTCTT ATATTGCAAG CTCCATCTCT ACTGGTGTGT GCATTTAATG 1820

ACATCTAACT ACAGATGCCG CACAGCCACA ATGCTTTGCC TTATAGTTTT 1870

TTAACTTTAG AACGGGATTA TCTTGTTATT ACCTGTATTT TCAGTTTCGG 1920

ATATTTTTGA CTTAATGATG AGATTATCAA GACGTACCCC TATGCTAAGT 1970

CATGAGCATA TGGACTTACG AGGGTTCGAC TTAGAGTTTT GAGCTTTAAG 2020

ATAGGATTAT TGGGGGCTTA CCCCCACCTT AATTAGAAGA AACATTTTAT 2070

ATTGCTTTAC TA 2082

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATAAAAGTT CCTGCACCAT GACCAGAGAC ACAGTGTGTC AGTGTAAAGA 50

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTTCAGGAAA CCAGAGCTTC CCTC 24

5

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs

10
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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TTCTCCCGTT TGCTTATCAC ACGC 24